04635186

2/24	3/24
4/24	5/24
6/24	7/24

Fig.1

```
-60   tgaaaagatagaataaatggcctcgtg

 1    ATGGCGCGGCCAGCGCTGCTGGGCGAG
 1     M   A   R   P   A   L   L   G   E

 61   GGCCAAGTTGCCGCGGCCACAGAAGTT
 21    G   Q   V   A   A   A   T   E   V

121   GAAAATCTCTGCACGATAATATGGACG
 41    E   N   L   C   T   I   I   W   T

181   ACTCTCAGATATTTTAGTCACTTTGAT
 61    T   L   R   Y   F   S   H   F   D

241   CATCGTAAAGAGGAATTACCCCTGGAT
 81    H   R   K   E   E   L   P   L   D

301   AGTGCCAATGAAAGTGAGAAGCCTAGC
101    S   A   N   E   S   E   K   P   S

361   GGTGATCCTGAGTCCGCTGTGACTGAG
121    G   D   P   E   S   A   V   T   E

421   AAGTGTTCCTGGCTCCCTGGAAGGAAT
141    K   C   S   W   L   P   G   R   N
```

Fig. IA

```
ccgaattcggcacgagccgaggcgagggcctgc

CTGTTGGTGCTGCTACTGTGGACCGCCACCGTG
 L  L  V  L  L  L  W  T  A  T  V

CAGCCACCTGTGACGAATTTGAGCGTCTCTGTC
 Q  P  P  V  T  N  L  S  V  S  V

TGGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
 W  S  P  P  E  G  A  S  P  N  C

GACCAACAGGATAAGAAAATTGCTCCAGAAACT
 D  Q  Q  D  K  K  I  A  P  E  T

GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
 E  K  I  C  L  Q  V  G  S  Q  C

CCTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
 P  L  V  K  K  C  I  S  P  P  E

CTCAAGTGCATTTGGCATAACCTGAGCTATATG
 L  K  C  I  W  H  N  L  S  Y  M

ACAAGCCCTGACACACACTATACTCTGTACTAT
 T  S  P  D  T  H  Y  T  L  Y  Y
```

Fig. IB

```
481   TGGTACAGCAGCCTGGACAAAAGTCGT
161    W  Y  S  S  L  E  K  S  R


541   ATTGCTTGTTCCTTTAAATTGACTAAA
181    I  A  C  S  F  K  L  T  K


601   ATAATGGTCAAGGATAATGCTGGGAAA
201    I  M  V  K  D  N  A  G  K


661   TCCTATGTGAAACCTGATCCTCCACAT
221    S  Y  V  K  P  D  P  P  H


721   TTAGTGCAGTGGAAGAATCCACAAAAT
241    L  V  Q  W  K  N  P  Q  N


781   GTCAATAATACTCAAACCGACCGACAT
261    V  N  N  T  Q  T  D  R  H


841   AATTCCGAATCTGATAGAAACATGGAG
281    N  S  E  S  D  R  N  M  E


901   GCCGACGCTGTCTACACAGTCAGAGTA
301    A  D  A  V  Y  T  V  R  V


961   AACAAACTGTGGAGTGATTGGAGTGAA
321    N  K  L  W  S  D  W  S  E
```

```
CAATGTGAAAACATCTATAGAGAAGGTCAACAC
 Q   C   E   N   I   Y   R   E   G   Q   H

GTGGAACCTAGTTTTGAACATCAGAACGTTCAA
 V   E   P   S   F   E   H   Q   N   V   Q

ATTAGGCCATCCTGCAAAATAGTGTCTTTAACT
 I   R   P   S   C   K   I   V   S   L   T

ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA
 I   K   H   L   L   L   K   N   G   A   L

TTTAGAAGCAGATGCTTAACTTATGAAGTGGAG
 F   R   S   R   C   L   T   Y   E   V   E

AATATTTTAGAGGTTGAAGAGGACAAATGCCAG
 N   I   L   E   V   E   E   D   K   C   Q

GGTACAAGTTGTTTCCAACTCCCTGGTGTTCTT
 G   T   S   C   F   Q   L   P   G   V   L

AGAGTCAAAACAAACAAGTTATGCTTTGATGAC
 R   V   K   T   N   K   L   C   F   D   D

GCACAGAGTATAGGTAAGGAGCAAAACTCCACC
 A   Q   S   I   G   K   E   Q   N   S   T
```

```
1021   TTCTACACCACCATGTTACTCACCATT
341     F   Y   T   T   M   L   L   T   I

1081   CTTTTTTACCTGAAAAGGCTTAAGATC
361     L   F   Y   L   K   R   L   K   I

1141   ATTTTTAAAGAAATGTTTGGAGACCAG
381     I   F   K   E   M   F   G   D   Q

1201   ATCTATGAGAAACAATCCAAAGAAGAA
401     I   Y   E   K   Q   S   K   E   E

1261   AAAGCAGCTCCTTGAtggggagaagtg
421     K   A   A   P   *

1321   gatttattgcattctccatttgttatc
1381   cttgaaaaacaggcagctcctaagagc
1441   ccaaacccaaaggagctccttccaaga
1501   ccctaaaagcagatgttttgccaaatc
1561   accatcaattcatctaatcaggaattg
```

Fig.IE

```
CCAGTCTTTGTCGCAGTGGCAGTCATAATCCTC
 P   V   F   V   A   V   A   V   I   I   L

ATTATATTTCCTCCAATTCCTGATCCTGGCAAG
 I   I   F   P   P   I   P   D   P   G   K

AATGATGATACCCTGCACTGGAAGAAGTATGAC
 N   D   D   T   L   H   W   K   K   Y   D

ACGGATTCTGTAGTGCTGATAGAAAACCTGAAG
 T   D   S   V   V   L   I   E   N   L   K

atttctttcttgccttcaatgtgaccctgtgaa


tggggacttgttaaatagaaactgaaactact
cacaggtcttgatgtgacttttgcattgaaaac
aaagcaagagttcttctcgttccttgttccaat
cccaaactagaggacaaagacaaggggacaatg
tgatggcttcctaggaatctctgcttgctctg
```

Fig. IF
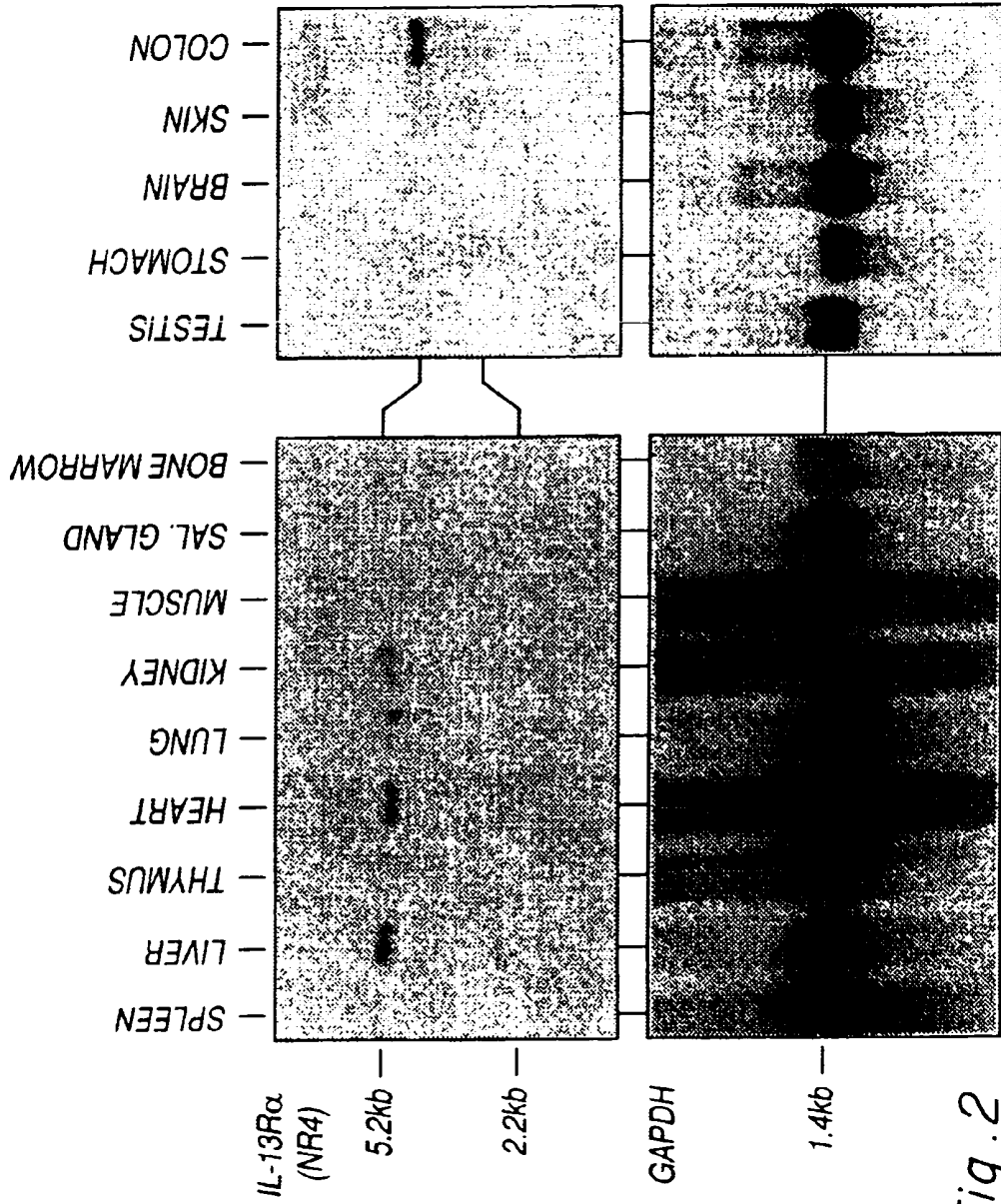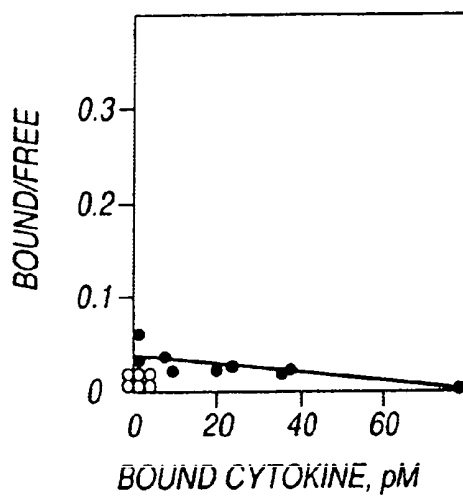
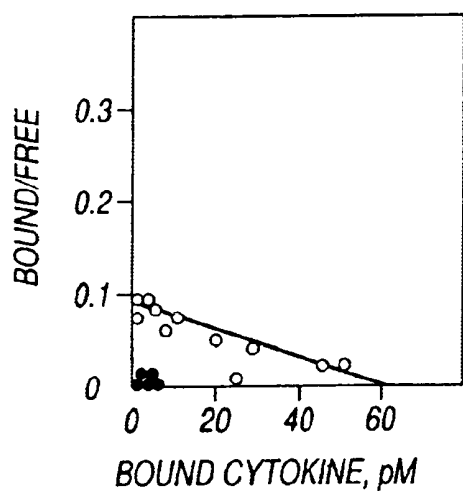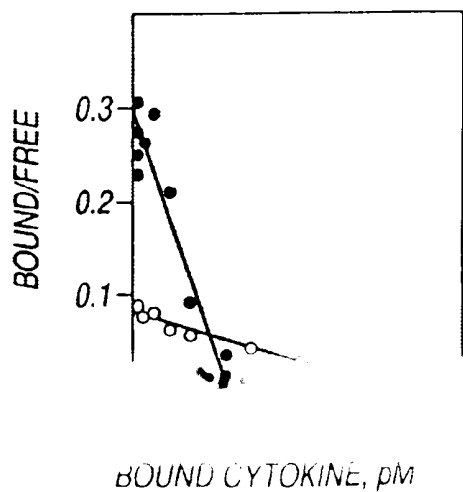NR4 EXPRESSION IN MOUSE TISSUES

Fig.2

Fig.3A

BOUND/FREE

BOUND CYTOKINE, pM

Fig.3B

BOUND/FREE

BOUND CYTOKINE, pM

Fig.3C

BOUND/FREE

BOUND CYTOKINE, pM

Fig.4A

(COMPETITOR), ng/ml

Fig.4B

(COMPETITOR), ng/ml
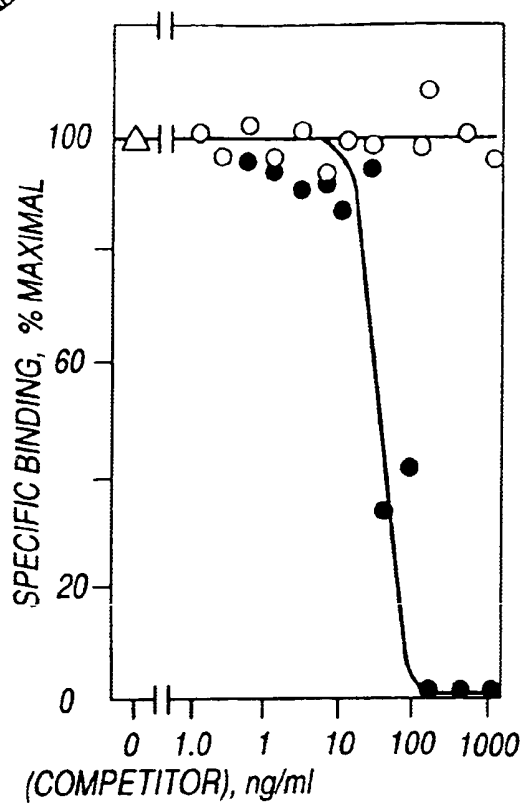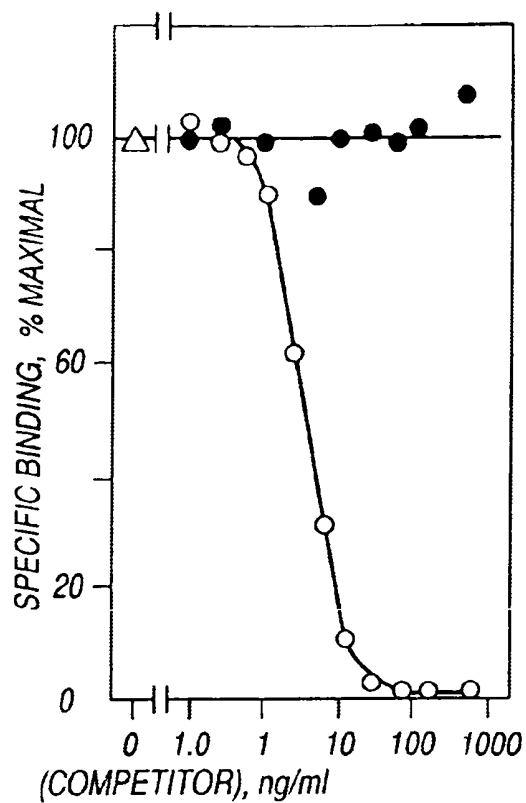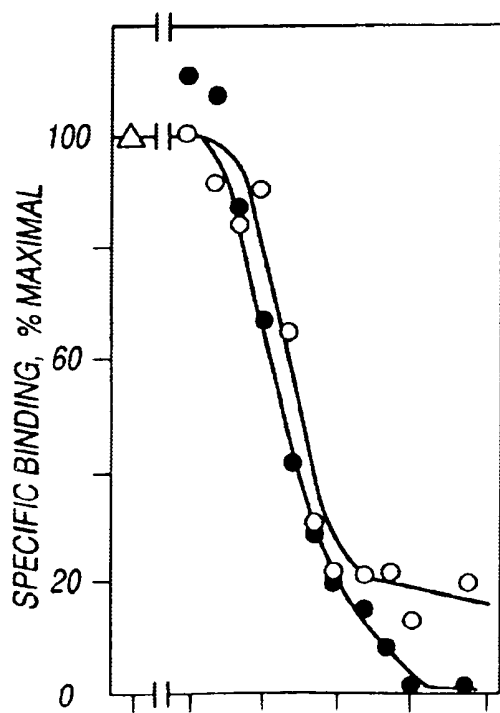
Fig.4C
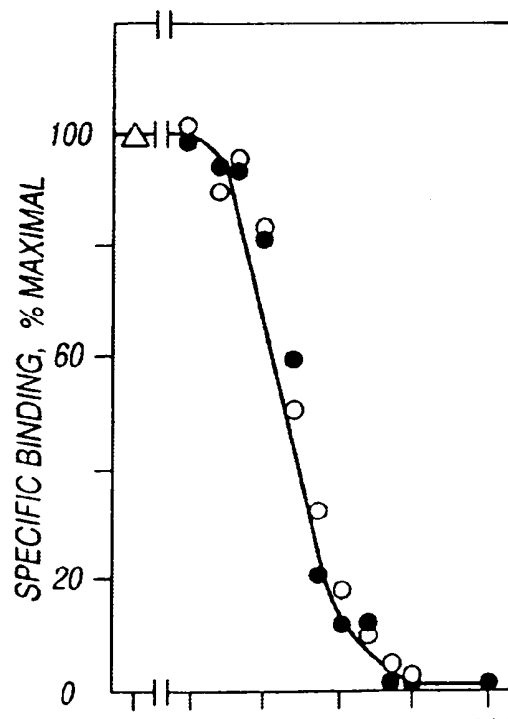
Fig.4D
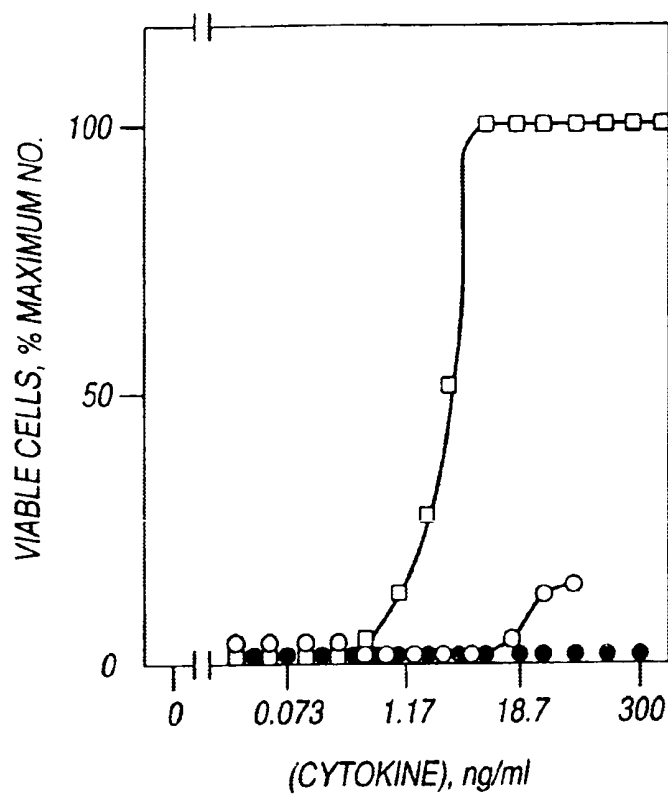
Fig.5A
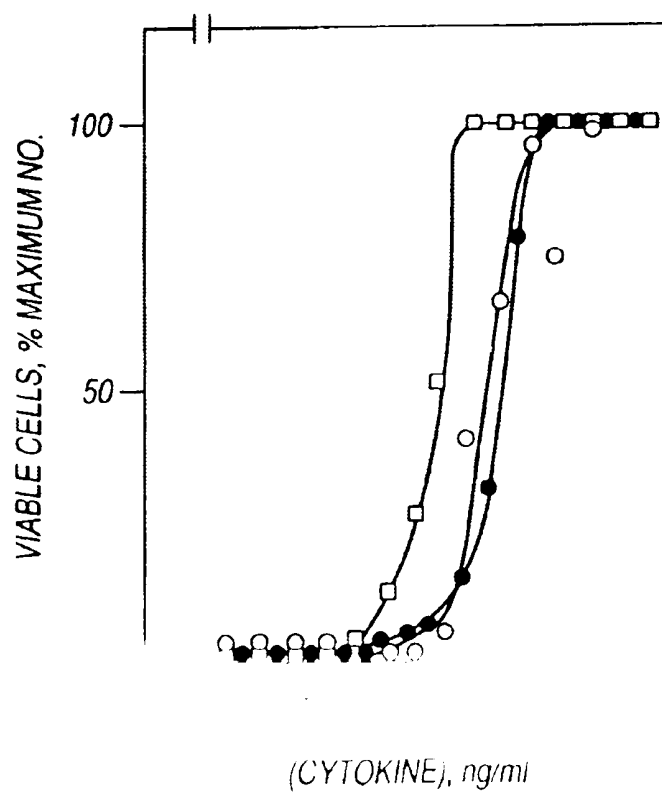
Fig.5B

CROSS-SPECIES CONSERVATION OF THE NR-4 (IL-13R α)
GENE

HORSE COW CHICKEN PIG RABBIT RAT SHEEP HUMAN DOG GUINEA PIG MOUSE

Kb

23.1

9.4

6.6

4.4

2.3
2.0
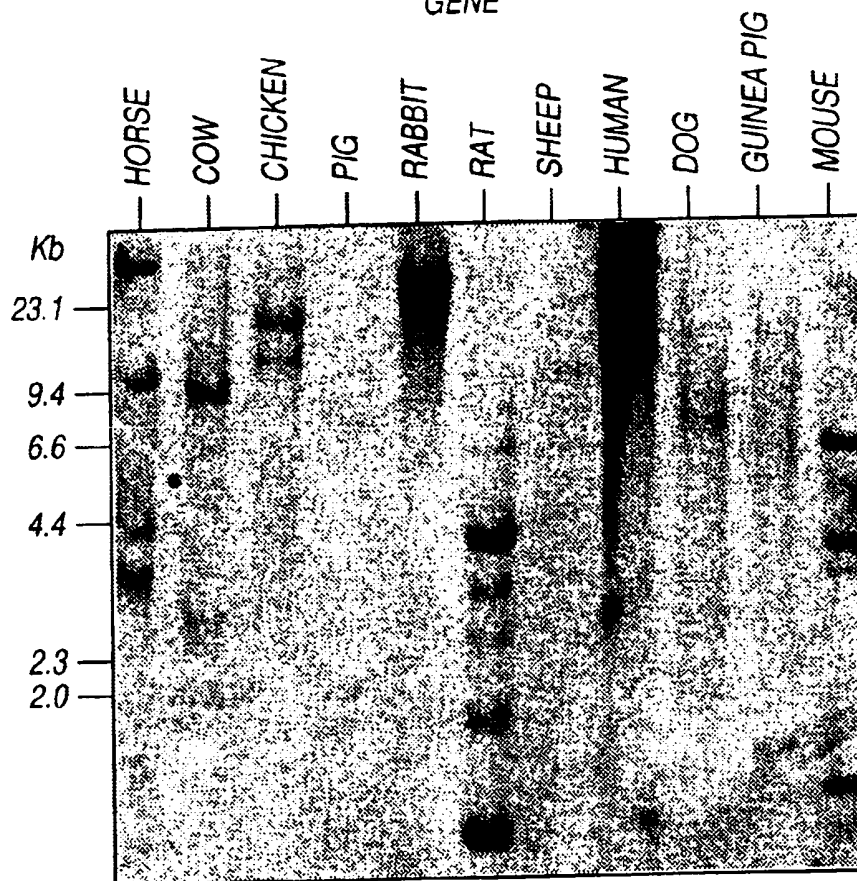
Fig. 6

(major)

DYKDD DDYKD DDESR TEVQP PVTXL SV
1   5   10   15   20   25

(minor)

ASTSS SDYKD DDESR TEVQP PVTXL SV

Fig. 10

14/24	15/24
16/24	17/24
18/24	19/24
20/24	21/24
22/24	23/24

```
H              gagtctaacacggaccaaggagtttaac

M    -60       tgaaaagatagaataaatggcctcgtgc

H              M   E   W   P   A   R   L   C   G
               ATGGAGTGGCCGGCGCGGCTCTGCGGGC
                *           *   *       *
M     1        ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M     1          M   A   R   P   A   L   L   G   E


H                G   G   G   G   A   P   T   E   T
H              GGGGGCGGGGGGCGCGCCTACGGAAACTC
                *               *       *   *
M     61       GGCCAAGTTGCCGCGGCCACAGAAGTTC
M     21         G   Q   V   A   A   A   T   E   V


H                E   N   L   C   T   V   I   W   T
H              GAAAACCTCTGCACAGTAATATGGACAT
                *   *   *   *   *       *   *   *
M    121       GAAAATCTCTGCACGATAATATGGACGT
M     41         E   N   L   C   T   I   I   W   T


H                S   L   W   Y   F   S   H   F   G
H              AGTCTATGGTATTTTAGTCATTTTGGCG
                    *       *   *   *   *   *
M    181       ACTCTCAGATATTTTAGTCACTTTGATG
M     61         T   L   R   Y   F   S   H   F   D
```

Fig 7A

```
acgtgcggccgggttccgaggcgagaggctgc
    ....        ..........  .  ....
cgaattcggcacgagccgaggcgagggcctgc


L   W   A   L   L   L   C   A   G   G   G   G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGC
*           *   *   *
TGTTGGTGCTGCTACTGTGGACCGCCACCGTG---
L   L   V   L   L   L   W   T   A   T   V   -


Q   P   P   V   T   N   L   S   V   S   V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT
*   *   *   *   *   *   *   *   *   *   *
AGCCACCTGTGACGAATTTGAGCGTCTCTGTC
Q   P   P   V   T   N   L   S   V   S   V


W   N   P   P   E   G   A   S   S   N   C
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT
*       *   *   *   *   *   *       *   *
GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
W   S   P   P   E   G   A   S   P   N   C


D   K   Q   D   K   K   I   A   P   E   T
ACAAACAAGATAAGAAAATAGCTCCGGAAACT
*       *   *   *   *   *   *   *   *   *
ACCAACAGGATAAGAAAATTGCTCCAGAAACT
D   Q   Q   D   K   K   I   A   P   E   T
```

Fig 7R

```
H           R   R   S   I   E   V   P   L   N
H           CGTCGTTCAATAGAAGTACCCCTGAATG
              *           *       *   *
M   241     CATCGTAAAGAGGAATTACCCCTGGATG
M    81     H   R   K   E   E   L   P   L   D


H               S   T   N   E   S   E   K   P   S
H               AGCACCAATGAGAGTGAGAAGCCTAGCA
                *       *   *   *   *   *   *   *
M   301         AGTGCCAATGAAAGTGAGAAGCCTAGCC
M   101         S   A   N   E   S   E   K   P   S


H               G   D   P   E   S   A   V   T   E
H               GGTGATCCTGAGTCTGCTGTGACTGAAC
                *   *   *   *   *   *   *   *   *
M   361         GGTGATCCTGAGTCCGCTGTGACTGAGC
M   121         G   D   P   E   S   A   V   T   E


H               K   C   S   W   L   P   G   R   N
H               AAGTGTTCTTGGCTCCCTGGAAGGAATA
                *   *   *   *   *   *   *   *   *
M   421         AAGTGTTCCTGGCTCCCTGGAAGGAATA
M   141         K   C   S   W   L   P   G   R   N


H               W   H   R   S   L   E   K   I   H
H               TGGCACAGAAGCCTGGAAAAAATTCATC
```

Fig 7C

```
E   R   I   C   L   Q   V   G   S   Q   C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
*       *   *   *   *   *   *   *   *   *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E   K   I   C   L   Q   V   G   S   Q   C


I   L   V   E   K   C   I   S   P   P   E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
    *   *   *   *   *   *   *   *   *   *
CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
P   L   V   K   K   C   I   S   P   P   E


L   Q   C   I   W   H   N   L   S   Y   M
TTCAATGCATTTGGCACAACCTGAGCTACATG
*       *   *   *   *   *   *   *   *   *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L   K   C   I   W   H   N   L   S   Y   M


T   S   P   D   T   N   Y   T   L   Y   Y
CCAGTCCCGACACTAACTATACTCTCTACTAT
*   *   *   *   *       *   *   *   *   *
CAAGCCCTGACACACACTATACTCTGTACTAT
T   S   P   D   T   H   Y   T   L   Y   Y


Q   C   E   N   I   F   R   E   G   Q   Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC
```

Fig. 7D

```
                *            *   *    *    *
M  481   TGGTACAGCAGCCTGGAGAAAAGTCGTC
M  161    W   Y   S   S   L   E   K   S   R

H         F   G   C   S   F   D   L   T   K
H        TTTGGTTGTTCCTTTGATCTGACCAAAG
               *   *   *        *   *    *
M  541   ATTGCTTGTTCCTTTAAATTGACTAAAG
M  181    I   A   C   S   F   K   L   T   K

H         Q   I   M   V   K   D   N   A   G
H        CAAATAATGGTCAAGGATAATGCAGGAA
          *   *   *   *   *   *   *   *   *
M  601   CAAATAATGGTCAAGGATAATGCTGGGA
M  201    Q   I   M   V   K   D   N   A   G

H         T   S   R   V   K   P   D   P   P
H        ACTTCCCGTGTGAAACCTGATCCTCCAC
          *   *       *   *   *   *   *   *
M  661   ACTTCCTATGTGAAACCTGATCCTCCAC
M  221    T   S   Y   V   K   P   D   P   P

H         L   Y   V   Q   W   E   N   P   Q
H        CTATATGTGCAATGGGAGAATCCACAGA
          *       *   *   *        *   *   *
M  721   TTATTAGTGCAGTGGAAGAATCCACAAA
M  241    L   L   V   Q   W   K   N   P   Q
```

Fig 7F

```
*    *    *    *    *         *    *    *    *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q   C   E   N   I   Y   R   E   G   Q   H


V   K   D   S   S   F   E   Q   H   S   V
TGAAGGATTCCAGTTTTGAACAACACAGTGTC
*                   *    *    *              *
TGGAACCT---AGTTTTGAACATCAGAACG TT
V   E   P   -   S   F   E   H   Q   N   V


K   I   K   P   S   F   N   I   V   P   L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
*    *         *    *              *    *         *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K   I   R   P   S   C   K   I   V   S   L


H   I   K   N   L   S   F   H   N   D   D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
*    *    *         *                   *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H   I   K   H   L   L   L   K   N   G   A


N   F   I   S   R   C   L   F   Y   E   V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
*    *         *    *    *    *         *    *    *
ATTTTAGAAGCAGATGCTTAACTTATGAAGTG
N   F   R   S   R   C   L   T   Y   E   V
```

Fig 7F

```
H                E   V   N   N   S   Q   T   E   T
H                GAAGTCAATAACAGCCAAACTGAGACAC
                 *   *   *   *       *   *
M   781          GAGGTCAATAATACTCAAACCGACCGAC
M   261          E   V   N   N   T   Q   T   D   R


H                    E   N   P   E   F   E   R   N   V
H                    GAGAATCCAGAATTTGAGAGAAATGTGG
                     *       *           *   *
M   841              CAGAATTCCGAATCTGATAGAAACATGG
M   281              Q   N   S   E   S   D   R   N   M


H                    L   P   D   T   L   N   T   V   R
H                    CTTCCTGATACTTTGAACACAGTCAGAA
                     *       *           *   *   *
M   901              CTTGCCGACGCTGTCTACACAGTCAGAG
M   301              L   A   D   A   V   Y   T   V   R


H                    D   D   K   L   W   S   N   W   S
H                    GATGACAAACTCTGGAGTAATTGGAGCC
                     *       *   *   *   *       *   *
M   961              GACAACAAACTGTGGAGTGATTGGAGTG
M   321              D   N   K   L   W   S   D   W   S


H                    T   L   Y   I   T   M   L   L   I
H                    ACACTCTACATAACCATGTTACTCATTG
```

Fig 7G

```
H   N   V   F   Y   V   Q   E   A   K   C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
*   *               *       *       *   *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H   N   I   L   E   V   E   E   D   K   C


E   N   T   S   C   F   M   V   P   G   V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
*       *   *   *   *           *   *   *
AGGGTACAAGTTGTTTCCAACTCCCTGGTGTT
E   G   T   S   C   F   Q   L   P   G   V


I   R   V   K   T   N   K   L   C   Y   E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
    *   *   *   *   *   *   *   *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V   R   V   K   T   N   K   L   C   F   D


Q   E   M   S   I   G   K   K   R   N   S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
        *   *   *   *           *   *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E   A   Q   S   I   G   K   E   Q   N   S


V   P   V   I   V   A   G   A   I   I   V
TTCCAGTCATCGTCGCAGGTGCAATCATAGTA
```

Fig 7H

```
                    *           *           *     *     *     *

M    1021   ACCTTCTACACCACCATGTTACTCACCA
M    341       T   F   Y   T   T   M   L   L   T

H               L   L   L   Y   L   K   R   L   K
H           CTCCTGCTTTACCTAAAAAGGCTCAAGA
                *   *       *     *     *     *     *     *

M    1081   CTCCTTTTTTACCTGAAAAGGCTTAAGA
M    361       L   L   F   Y   L   K   R   L   K

H               K   I   F   K   E   M   F   G   D
H           AAGATTTTTAAAGAAATGTTTGGAGACC
                *   *   *   *   *   *   *   *   *

M    1141   AAGATTTTTAAAGAAATGTTTGGAGACC
M    381       K   I   F   K   E   M   F   G   D

H               D   I   Y   E   K   Q   T   K   E
H           GACATCTATGAGAAGCAAACCAAGGAGG
                *   *   *   *   *   *       *   *

M    1201   GACATCTATGAGAAACAATCCAAAGAAG
M    401       D   I   Y   E   K   Q   S   K   E

H               K   K   A   S   Q   *
H           AAGAAAGCCTCTCAGTGAtggagataat
                *   *   *

M    1261   AAGAAAGCAGCTCCTTGAtggggagaag
M    421       K   K   A   A   P   *
```

Fig.71

```
         *       *          *       *          *          *
TTCCAGTCTTTGTCGCAGTGGCAGTCATAATC
I   P   V   F   V   A   V   A   V   I   I


I   I   I   F   P   P   I   P   D   P   G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
*   *   *   *   *   *   *   *   *   *   *
TCATTATATTTCCTCCAATTCCTGATCCTGGC
I   I   I   F   P   P   I   P   D   P   G


Q   N   D   D   T   L   H   W   K   K   Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
*   *   *   *   *   *   *   *   *   *   *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q   N   D   D   T   L   H   W   K   K   Y


E   T   D   S   V   V   L   I   E   N   L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
*   *   *   *   *   *   *   *   *   *   *
AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E   T   D   S   V   V   L   I   E   N   L


ttattttttaccttcactgtgaccttgagaaga

tgatttctttcttgccttcaatgtgaccctgt
```
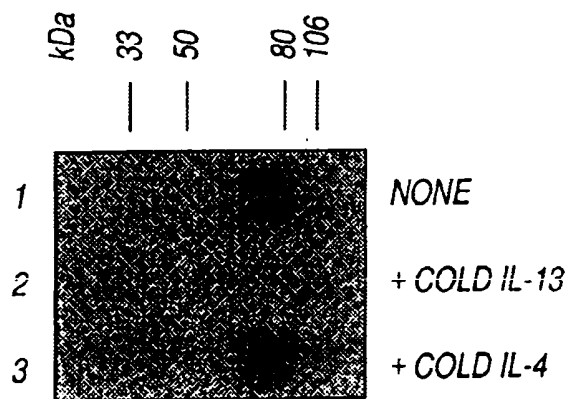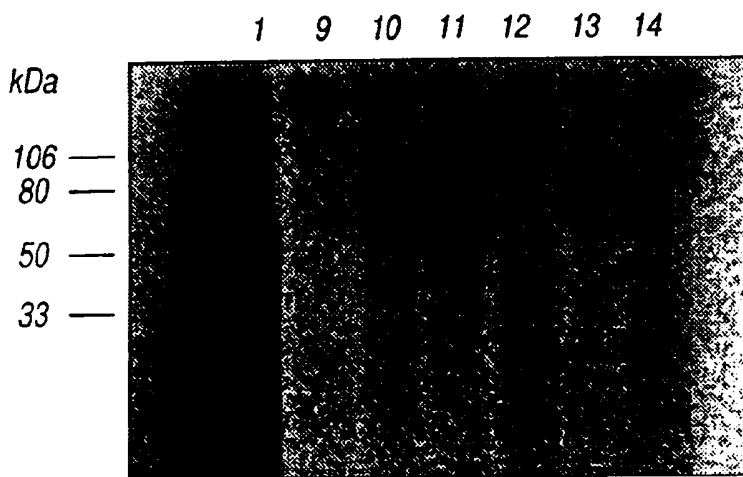
Fig. 7J

Fig.8

Fig.9